

FIGURE

1a 1b

C1a/C1b	
MASP-2	TPGPPHKEPVGNLSPYKQETANDGERRMTLTAPQYTLRLYFTHFOLESHLSEYDFVLLSGARVLATLQDQSTDTERRAPKDT 90
MASP-1	HTVELNHHFQIQSPGYPOSTPEDEFTVWMTVPDGFRIKLYFVFNHLESSYLSEYDYVKEVTEQVLAFFQCAETDTTEQTPQGEV 87
C1c	SIPFQKLPGVETSLPPKPYFPHFETTVITVPTOTREVELVFQPDLEPSECEFTDYVLSADKKSLGNFQQLGSLGNPPCKEKE 87
C1a	EPHYGELISPHYPOATPSEVESLWDIEVPEDYTNLYFTHLQISENCAVDSVQLISGOTTEKRLQDQRESNHPKSPIVES 83
SGF	
MASP-2	FVSLGSSLDITERSDYSENEERETGPRFYAARDIDEGQVAPCEAPTCDHMQNNLGGFYCESRAGTYVLHNNKATCSALCS 170
MASP-1	VLEPGSPHSTTPRSDYSENEERETGPRFYAARDIDEGQVAPCEAPTCDHMQNNLGGFYCESRAGTYVLHNNKATCSALCS 167
C1c	FNSQCHNLLTPHTDPSNEEDNTHPYKFLAYYQAVGLDECAERSKSGEDPOPOQDMLQWYVGGVYFCELPYFLOESNHSQAGAS 177
C1a	FQVPYKLVIFASDYSENEERETGPRFYAARDIDEGQVAPCEAPTCDHMQNNLGGFYCESRAGTYVLHNNKATCSALCS 163
C1c/C1a	
MASP-2	GOVPTORSGELSSPEYFPRPYKLSNCTYSISLEQFVILDVYSSDYVETNPTLGEPTDPLKIGTDREHNPPECKTLPHR 1278 256
MASP-1	DNLTORTOVITSPOFPHYFKSSECLYTLLESGFNNLOFSDIPIEDNPEVPEPTDYIKLVQPKVLPQPEKAPEP 1270S 253
C1c	SKLTYEASGYISLEYPREYFPOLKQYSIRVERGLTLHLKFLKFPIDDMQVHCEPTDQLQYANGKHICEFCOKRPPD 1273S 263
C1a	GOVPTALDGIASPHYKPYVPEISCEYQVILEKGFQVVTLERETQVEMADEAGNQLSLVFAVAGROFQYQNGPFPPLMIEYS 250
CEP-1	
MASP-2	NTVITTPVDSGCHTQNKINHTTSTAQCPYFPHAPPHGIVSPVQKYLKQSFIPSTOTYELLQHLPLKSTAVQKQDCAWDRPRA 345
MASP-1	HSVLPHNSDNGENKRLSYRAAGCEPELOPPVHGNIEPQAKYFFKQVLSCTGYKVLKQNVENOTFQICLQDQTHSKIPT 342
C1c	NAVOLLPTDSEGLSCKNKLRYTTRIKQPKETLQETIIONLQIYQFADYFINTQKQYGLIECHQVLSFTAVQDQDQTHIRANR 353
C1a	NALDIFQDGLQKAGKLAHGDHPCPKEDTPNVMPEAKRYVFRVVOITLQGFVVEGRVQATSPYSTQSNHNRNSKLE 338
CCP-2	
MASP-2	CSIVDQPPDDLPSGRVYITGROVYIKAVIQSCEETPYTHXVNDQKYVCEADQNTSSRGEKELPVCEPVCLSLARTT 426
MASP-1	CKIVDQAPGELSGELIYSTRNNLTYSKSIKYSQCEPYTHLNNHTCIYTCAGGVNHHVGLKELPTLPVQDLPHPSKEL 426
C1c	CKIKDQDQPNLNGOPRYTTTNGVNTYKALIGYTCHEPYTHNTRAGSRISQGVYTCAGGVNHHVGLKELPTLPVQDLPHPSKEL 443
C1a	QGVVQDQIPESIEHGVKEDPESTLVGSVYITQCEPYTHNNGGGEYHCGAGHSHVHVLGPELPEGVVQGVPRPEE 419
serine protease	
MASP-2	QGRIVGQKARPGQFPVQLVILQGTFAAGALLYNNVLTAAAVYTEQKDAALDITKGLKRLSPHYTQNSAEPVTHG 507
MASP-1	KARIVNORPAQKOTTPHMLSHLNGQFCCSILLGSSNIVTAAKLNQSLQKPTLQDLSLSPDPRITLQKNNKLSGNEQHLG 515
C1c	RQRIGGQKAGHNPVQVFTNINRGCGALLGDRNLTAAHTLYPKEAQSASLQVPLGHTNVEELNKLGNHP 523
C1a	KORIGGSDADIKHNPVQVFTNINRGCGALLGDRNLTAAHTLYPKEAQSASLQVPLGHTNVEELNKLGNHP 498
Linker	
MASP-2	YTHDAGFONDALIKLNNVIVNSHTPQLPKKAAEFMTDIDGTASGWLQRTGFLAHLNMYDIPVONKQCTAAYEK 589
MASP-1	VKHITLHPKYPDPTFENDVALVLESLPVLAAPVNPICLPQPOQDANVIVSGHQRFLQFETLHEIETPVONSTOQKAY 599
C1c	SVHPDYQDESYNFEDDIALLEHNSVTLQPLLPICLPQNDTPYDGLNGVYSGFVNHKEIANGKLPVLPVAPQADEN 608
C1a	KRLLEVPEGATNFONDIALVRLKDPVNGPTVSPICLPQTSDDYVLDQDLGLISGNGATEKRDRAVRLKAAALPVAPLAKREVKVE 586
Linker	
MASP-2	PPYPRGSVTANMLCAQLESCKGSCSGDGLALVPLDSETERAFVGVIVSGHNGEAGQYGVYTKVINYIPNINISDP 671
MASP-1	APLKKKVTREHICAEKEGKQDACSQSGGPPVTLNRERGCYLVUTVSHWDQCKKDRYGVYVYINQKDNQVTVTVN 680
C1c	CKNRNDVFGQNHFCAGKHSKQDACSQSGGVFAVRDPNDRVATGIVSHGICSGAGYGVYTKVINYIPNINISDP 688
C1a	KPTADAAVYVTPNTHCAGGKCHDSGKQSGGAFVQOPHDKTFYAAGLVSHGPOGTYGLYTRVINYVDMINKNENSTPRD 673

FIGURE

2

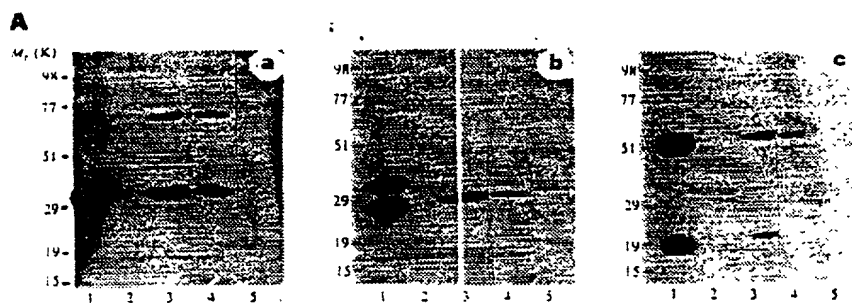
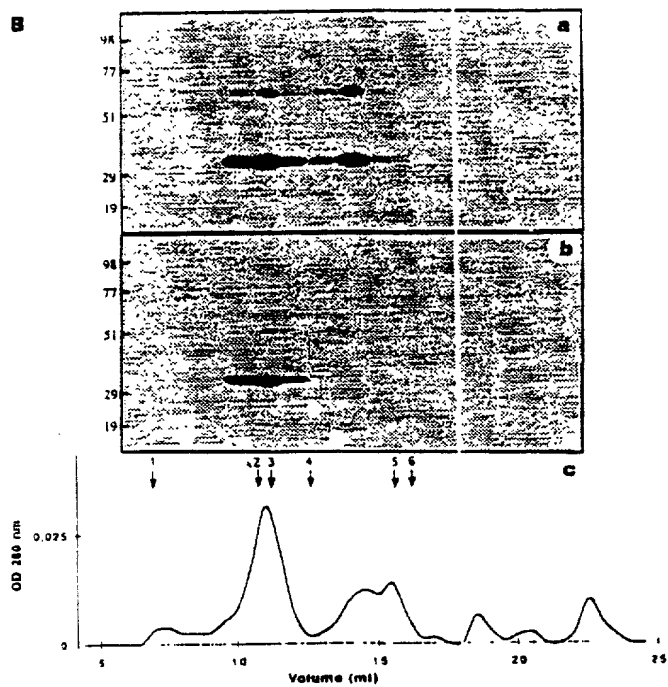
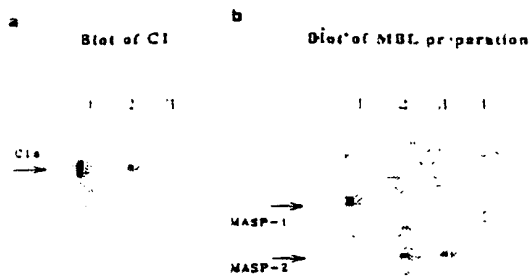


FIGURE 3A



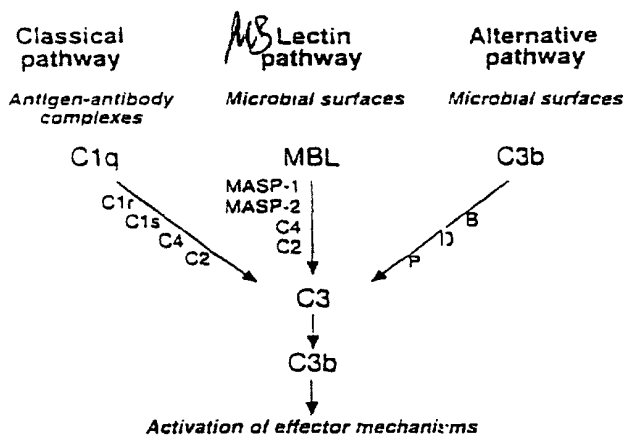
FIGURE

3B



FIGURE

4 a & b



FIGURE

5

+1

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 Fig. 6